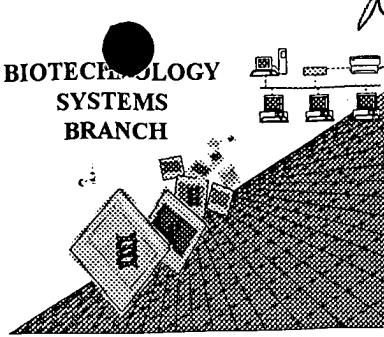


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/829,066
Source: O1PE
Date Processed by STIC: 4/30/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/829,066</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleics	<p>The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".</p>	
2 <input type="checkbox"/> Wrapped Aminos	<p>The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".</p>	
3 <input type="checkbox"/> Incorrect Line Length	<p>The rules require that a line not exceed 72 characters in length. This includes spaces.</p>	
4 <input type="checkbox"/> Misaligned Amino Acid Numbering	<p>The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.</p>	
5 <input type="checkbox"/> Non-ASCII	<p>This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.</p>	
6 <input type="checkbox"/> Variable Length	<p>Sequence(s) <input type="checkbox"/> contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.</p>	
7 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	<p>A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) <input type="checkbox"/>. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.</p>	
8 <input type="checkbox"/> Skipped Sequences (OLD RULES)	<p>Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped</p> <p>Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).</p>	
9 <input type="checkbox"/> Skipped Sequences (NEW RULES)	<p>Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000</p>	
10 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	<p>Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.</p>	
11 <input type="checkbox"/> Use of "Artificial" (NEW RULES)	<p>Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.</p>	
12 <input type="checkbox"/> Use of <220>Feature (NEW RULES)	<p>Sequence(s) <input type="checkbox"/> are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)</p>	
13 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	<p>Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.</p>	

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/829,066

DATE: 04/30/2001
TIME: 09:04:24

Input Set : A:\seqlist-09424800001.txt
Output Set: N:\CRF3\04302001\I829066.raw

Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: Nisson, Paul
5 Jesse, Joel
6 Li, Wu-bo
8 <120> TITLE OF INVENTION: Method for Isolating and Recovering Target DNA or RNA
Molecules Having
9 a Desired Nucleotide Sequence
11 <130> FILE REFERENCE: 0942.4800002
W--> 14 <140> CURRENT APPLICATION NUMBER: US/09/829,066
14 <141> CURRENT FILING DATE: 2001-04-10
16 <150> PRIOR APPLICATION NUMBER: US 09/103,577
17 <151> PRIOR FILING DATE: 1998-06-24
19 <160> NUMBER OF SEQ ID NOS: 11
21 <170> SOFTWARE: PatentIn version 3.0
25 <210> SEQ ID. NO: 1
26 <211> LENGTH: 23 *invalid - Per 1.823 of Sequence Rules, the only valid*
27 <212> TYPE: DNA
28 <213> ORGANISM: Oligonucleotide/Primer *(global error)*
30 <220> FEATURE:
31 <221> NAME/KEY: misc_feature
32 <222> LOCATION: 3
33 <223> OTHER INFORMATION: N is G, T, A, or C
35 <220> FEATURE:
36 <221> NAME/KEY: misc_feature
37 <222> LOCATION: 6
38 <223> OTHER INFORMATION: Y is C or T
40 <220> FEATURE:
41 <221> NAME/KEY: misc_feature
42 <222> LOCATION: 9
43 <223> OTHER INFORMATION: Y is C or T
45 <220> FEATURE:
46 <221> NAME/KEY: misc_feature
47 <222> LOCATION: 12
48 <223> OTHER INFORMATION: N is G, T, A, or C
50 <220> FEATURE:
51 <221> NAME/KEY: misc_feature
52 <222> LOCATION: 15
53 <223> OTHER INFORMATION: Y is C or T
55 <220> FEATURE:
56 <221> NAME/KEY: misc_feature
57 <222> LOCATION: 18
58 <223> OTHER INFORMATION: Y is C or T
60 <220> FEATURE:
61 <221> NAME/KEY: misc_feature
62 <222> LOCATION: 21
63 <223> OTHER INFORMATION: N is G, T, A, or C
66 <400> SEQUENCE: 1
W--> 67 gtrtgygayg gnttgcaygt ngg
71 <210> SEQ ID NO: 2

invalid - Per 1.823 of Sequence Rules, the only valid
<213> responses are: Unknown,
Artificial Sequence, or
Scientific name

(genus/species)

(one of the three)

see circled portion
of item 12 on Error
Summary Sheet

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/829,066

DATE: 04/30/2001
TIME: 09:04:24

Input Set : A:\seqlist-09424800001.txt
Output Set: N:\CRF3\04302001\I829066.raw

72 <211> LENGTH: 19
73 <212> TYPE: DNA
74 <213> ORGANISM: Oligonucleotide/Primer
77 <400> SEQUENCE: 2
78 gktggaggk ttcagtkgg 19
82 <210> SEQ ID NO: 3
83 <211> LENGTH: 18
84 <212> TYPE: DNA
85 <213> ORGANISM: Oligonucleotide/Primer
88 <400> SEQUENCE: 3
89 gktggaggk ttcagtg 18
93 <210> SEQ ID NO: 4
94 <211> LENGTH: 18
95 <212> TYPE: DNA
96 <213> ORGANISM: Oligonucleotide/Primer
99 <400> SEQUENCE: 4
100 gktggagggt tcagtkgg 18
104 <210> SEQ ID NO: 5
105 <211> LENGTH: 18
106 <212> TYPE: DNA
107 <213> ORGANISM: Oligonucleotide/Primer
111 <400> SEQUENCE: 5
112 gttggaggkt tcagtkgg 18
116 <210> SEQ ID NO: 6
117 <211> LENGTH: 17
118 <212> TYPE: DNA
119 <213> ORGANISM: Oligonucleotide/Primer
123 <400> SEQUENCE: 6
124 gttggaggkt tcagtg 17
128 <210> SEQ ID NO: 7
129 <211> LENGTH: 17
130 <212> TYPE: DNA
131 <213> ORGANISM: Oligonucleotide/Primer
135 <400> SEQUENCE: 7
136 gktggagggt tcagtg 17
140 <210> SEQ ID NO: 8
141 <211> LENGTH: 17
142 <212> TYPE: DNA
143 <213> ORGANISM: Oligonucleotide/Primer
147 <400> SEQUENCE: 8
148 gttggagggt cagtkgg 17
152 <210> SEQ ID NO: 9
153 <211> LENGTH: 16
154 <212> TYPE: DNA
155 <213> ORGANISM: Oligonucleotide/Primer
157 <400> SEQUENCE: 9
158 gttggagggt cagtgg 16
162 <210> SEQ ID NO: 10
163 <211> LENGTH: 25

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/829,066

DATE: 04/30/2001
TIME: 09:04:24

Input Set : A:\seqlist-09424800001.txt
Output Set: N:\CRF3\04302001\I829066.raw

164 <212> TYPE: DNA
165 <213> ORGANISM: Oligonucleotide/Primer
167 <400> SEQUENCE: 10
168 gaccgttcag ctggatatta cggcc
172 <210> SEQ ID NO: 11
173 <211> LENGTH: 13
174 <212> TYPE: DNA
175 <213> ORGANISM: Oligonucleotide/Primer
176 <223> OTHER INFORMATION: consensus sequence for initiation of translation
179 <400> SEQUENCE: 11
180 gccgccagcc aug

25

13

insert this
7<2207> mandatory
remove
identifier
whenever
7<2217><2227>
or <2237>
shown.

<2207 never
has a response;
it is a "header"
only.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/829,066

DATE: 04/30/2001

TIME: 09:04:25

Input Set : A:\seqlist-09424800001.txt
Output Set: N:\CRF3\04302001\I829066.raw

L:14 M:282 W: Numeric Field Identifier Missing, <140> CURRENT APPLICATION NUMBER: is Added.
L:67 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1